In the specification

1.   Please Amend Table 2B on page 28 as follows:

Table 2B   Polymerase Domain Mutations in Various DNA Polymerases

Enzyme	Domain (bp)	Domain sequence	Predicted Mutations for Reducing DNA Polymerase Activity#
	DXXSLYP		
Pfu	405-411	DFRALYP	D405 (D405E)
Tgo	404-410	DFRSLYP	D404 (D404E)
KOD	404-410	DFRSLYP	D404 (D404E)
Vent	407-413	DFRSLYP	D407 [(D404E)]D407E
Deep Vent	405-411	DFRSLYP	D405 [(D404E)]D405E
	YXDTDS		
Pfu	539-544	YIDTDG	T542, D543 (T542P; D543G)
Tgo	538-543	YADTDG	T541, D542 (T541P; D542G)
KOD	538-543	YSDTDG	T541, D542 (T541P; D542G)
Vent	541-546	YADTDG	T544, D545 (T544P; D545G)
Deep Vent	539-544	YIDTDG	T542, D543 (T542P; D543G)
	KXY		
Pfu	593-595	KRY	K593 (K593T)
Tgo	592-594	KKY	K592 (K592T)
KOD	592-594	KKY	K592 (K592T)
Vent	595-597	KRY	K595 (K595T)
Deep			

Vent	593-595	KKY	K593 (K593T)

2. On page 19, before the full paragraph starting with "Enzymes possessing 3'-5' exonuclease activity" and ends with "Preferably, the enzyme comprising 3'-5' exonuclease activity is a DNA polymerase," please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
1             5                 10                15

Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
            20                25                30

Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
            35                40                45

Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
    50                55                60

Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65                70                75                80

Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
                85                90                95

Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
            100               105               110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115               120               125

Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
    130               135               140

Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145               150               155               160
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Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile

                  165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys

              180   185   190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr

              195   200   205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu

              210   215   220

Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys

225   230   235   240

Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val

              245   250   255

His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr

              260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu

              275   280   285

Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly

              290   295   300

Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr

305   310   315   320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu

              325   330   335

Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu

              340   345   350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala

              355   360   365

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr

    370   375   380

Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile

385   390   395   400

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His

            405   410   415

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp

          420   425   430

Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe

          435   440   445

Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys

    450   455   460

Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp

465   470   475   480

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr

          485   490   495

Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser

          500   505   510

Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu

          515   520   525

Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu

    530   535   540

His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545   550   555   560

Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu

          565   570   575

Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys

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               580                      585                      590
Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu
           595                      600                      605
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
       610                      615                      620
Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val
625 .                      630                      635                      640
Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
                   645                      650                      655
Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp
               660                      665                      670
Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala
           675                      680                      685
Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
       690                      695                      700
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
705                      710                      715                      720
Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
                   725                      730                      735
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
               740                      745                      750
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
           755                      760                      765
Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10)
       770                      775
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--Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

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atgatccttg  acgttgatta  catcaccgag  aatggaaagc  ccgtcatcag  ggtcttcaag      60

aaggagaacg  gcgagttcag  gattgaatac  gaccgcgagt  tcgagcccta  cttctacgcg     120

ctcctcaggg  acgactctgc  catcgaagaa  atcaaaaaga  taaccgcgga  gaggcacggc     180

agggtcgtta  aggttaagcg  cgcggagaag  gtgaagaaaa  agttcctcgg  caggtctgtg     240

gaggtctggg  tcctctactt  cacgcacccg  caggacgttc  cggcaatccg  cgacaaaata     300

aggaagcacc  ccgcggtcat  cgacatctac  gagtacgaca  tacccttcgc  caagcgctac     360

ctcatagaca  agggcctaat  cccgatggaa  ggtgaggaag  agcttaaact  catgtccttc     420

gacatcgaga  cgctctacca  cgagggagaa  gagtttggaa  ccgggccgat  tctgatgata     480

agctacgccg  atgaaagcga  ggcgcgcgtg  ataacctgga  agaagatcga  ccttccttac     540

gttgaggttg  tctccaccga  gaaggagatg  attaagcgct  tcttgagggt  cgttaaggag     600

aaggacccgg  acgtgctgat  aacatacaac  ggcgacaact  tcgacttcgc  ctacctgaaa     660

aagcgctgtg  agaagcttgg  cgtgagcttt  accctcggga  gggacgggag  cgagccgaag     720

atacagcgca  tggggacag  gtttgcggtc  gaggtgaagg  cagggtaca  cttcgacctt     780

tatccagtca  taaggcgcac  cataaacctc  ccgacctaca  cccttgaggc  tgtatacgag     840

gcggttttcg  gcaagcccaa  ggagaaggtc  tacgccgagg  agatagccac  cgcctgggag     900

accggcgagg  ggcttgagag  ggtcgcgcgc  tactcgatgg  aggacgcgag  ggttacctac     960

gagcttggca  gggagttctt  cccgatggag  gcccagcttt  ccaggctcat  cggccaaggc    1020

ctctgggacg  tttcccgctc  cagcaccggc  aacctcgtcg  agtggttcct  cctaaggaag    1080

gcctacgaga  ggaacgaact  cgctcccaac  aagcccgacg  agagggagct  ggcgaggaga    1140

agggggggct  acgccggtgg  ctacgtcaag  gagccggagc  ggggactgtg  ggacaatatc    1200

gtgtatctag  actttcgtag  tctctaccct  tcaatcataa  tcacccacaa  cgtctcgcca    1260

gatacgctca  accgcgaggg  gtgtaggagc  tacgacgttg  cccccgaggt  cggtcacaag    1320

ttctgcaagg  acttccccgg  cttcattccg  agcctgctcg  gaaacctgct  ggaggaaagg    1380

cagaagataa  agaggaagat  gaaggcaact  ctcgacccgc  tggagaagaa  tctcctcgat    1440

tacaggcaac  gcgccatcaa  gattctcgcc  aacagctact  acggctacta  cggctatgcc    1500

agggcaagat  ggtactgcag  ggagtgcgcc  gagagcgtta  cggcatgggg  aagggagtac    1560
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atcgaaatgg tcatcagaga gcttgaggaa aagttcggtt ttaaagtcct ctatgcagac   1620

acagacggtc tccatgccac cattcctgga gcggacgctg aaacagtcaa gaaaaaggca   1680

atggagttct taaactatat caatcccaaa ctgcccggcc ttctcgaact cgaatacgag   1740

ggcttctacg tcaggggctt cttcgtcacg aagaaaaagt acgcggtcat cgacgaggag   1800

ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag   1860

gagacgcagg cgagggtttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc   1920

agaattgtca gggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg   1980

gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta   2040

gccatagcga agcgtttggc cgccagaggt gttaaaatcc ggcccggaac tgtgataagc   2100

tacatcgttc tgaagggctc cggaaggata ggcgacaggg cgattccctt cgacgagttc   2160

gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgccggca   2220

gttgagagaa tcctcagggc cttcggctac cgcaaggaag acctgcgcta ccagaagacg   2280

aggcaggtcg ggcttggcgc gtggctgaag ccgaagggga agaagaagtg a 2331 (SEQ ID NO: 11)
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